

<!--StartFragment-->RESULT 2

S52984

catechol oxidase (EC 1.10.3.1) precursor - apple tree

N;Alternate names: polyphenol oxidase

C;Species: Malus domestica (apple tree)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004

C;Accession: S52984

R;Boss, P.K.; Gardner, R.C.; Janssen, B.J.; Ross, G.S.

Plant Mol. Biol. 27, 429-433, 1995

A;Title: An apple polyphenol oxidase cDNA is up-regulated in wounded tissues.

A;Reference number: S52984; MUID:95195170; PMID:7888632

A;Accession: S52984

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-593 <BOS>

A;Cross-references: UNIPROT:P43309; UNIPARC:UPI00001320F0; EMBL:L29450; NID:g507279; P

C;Superfamily: polyphenol oxidase, plant type

C;Keywords: chloroplast; copper; metalloprotein; oxidoreductase

F;196,205/Binding site: copper (His) #status predicted

F;327,331,361/Binding site: copper (His) #status predicted

Query Match 41.4%; Score 1343; DB 1; Length 593;

Best Local Similarity 46.0%; Pred. No. 4.7e-95;

Matches 291; Conservative 88; Mismatches 183; Indels 70; Gaps 21;

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Qy      1 MASLALSSLPTSTT---TKKPL--FSKTSSHV----KPFHRF--KVSCNAPADNNDKTVN 49
      | ||:  : | |      ||| ||: : | |      ||  | |||  | ||:  |
Db      1 MTSLSPPVVTTPVPNPATKPLSPFSQNNQVSLLTkPKRSFARKVSCK--ATNNDQ--N 56

Qy     50 NSDTPKLILPKTPLETQNVDRRNLGLGLGLYGAANLTTIPSAFGIPIAAPDNISDCVAA 109
      :   ||      ||||:||||||| | : | | | | | || | | : | | |
Db     57 DQAQSKL-----DRRNVLLGLGLYGVAGMGTDPFAPAKPIAPPD-VSKCGPA 103

Qy    110 TSNLRNSKDAIRGLA---CCPPVLSTNKPMDEVLPSPNVIRVRPAAQKATADYTAKYQQA 166
      | : |      ||| | : | : | : | : | : | : | : | : | : |
Db    104 -----DLPQGAVPTNCCPP--PSTKIIDFKLPAPAKLRIRPEAHAVDQAYRDKYKA 153

Qy    167 IQAMKDLPEDHPHSWKQGGKIHCAYCNGGYNQEQSGYPNLQLQIHNSWLFFPFHRWYLYF 226
      : : || ||: | | : ||| : ||||: | | : | : | : ||||| : |||
Db    154 MELMKALPDDDPKQQAQAAVHCAYCDGAY--DQVGFPELELQIHNSWLFFPFHRYLYF 211

Qy    227 YEKILGKLINDPTFALPYWNWDNPTGMVIPAMFEQNSKTNLFDPLRDAKHLPPSIFDVE 286
      : ||||| : ||||| : ||| : ||| : | : | : | : | : | : | : |
Db    212 FEKILGKLINDPTFALPFWNWDSPAGMPLPAIYA--DPKSPLYDKLRSANHQPTLVLDL 269

Qy    287 YAGADTGATCIDQIAINLSSMYRQMVNTSTDKRFFGGEFVAGNDPLASEFNVAGTVEAG 346
      | | :  :  | | ||||| : | : | | : ||: | | : | : |
Db    270 YNGTEDNVSKETTINANLKIMYRQMVNSKNAKLFFGNPYRAGDEPDG----GGSIEGT 325

Qy    347 VHTAAHRWVGNSRMANSEDMGNFYSGYDPLFYVHHANVDRMWQIWKDIDKKTHKDPTSG 406
      |  | | | : :  | ||||| ||: | : ||: |||| | | :  | | |
Db    326 PHAPVHLWTGDNTQPNFEDMGNFYSAGRDPFFAHHSNVDRMWSIWKTGGK-RTDLTDS 384

Qy    407 DWLNASYVIFYDENENLVRVYNRDCVDINRMGYDYERSAIPWIRSRPTAH-----AK 457
      |||: : : ||: || ||| |||: : || | : ||| : | : ||
Db    385 DWLDSGFLFYENAEELVRVKVRDCLETKNLGYVYQVDIPWLSSKPTPRRAKVALSKVAK 444

Qy    458 GANVA-----AKSAGIVQKVEDIVFPLKLNKIVKVLVKRP-ATNRTKEGKEKANELLFVNG 512
      ||  | | : : | | ||: | : : |||| | : | | | : | : |
Db    445 KLGVAHAHAVASSKVVAGTE---FPISLGSKISTVVKRPKQKKRSKAKEDDEEILVIEG 501

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Qy 513 ITFDAERFLKIDVFVNDVDDGIQTTAADSEFAGSFAQLPHNHGDKMFMRSAAFGITELL 572
| | | : : | | : | | | | : : : | | | | : | | : | : | |
Db 502 IEFDRDVAVKFDVYVNDVDD-LPSGPDKTEFAGSFVSVPHSHKHKKKMNTILRLGLTDLL 560
Qy 573 EDIEAEGDDSVVVTLVPRTGCDEVTIGEIKIQ 604
| : | | | | | | | | | : | | | | | :
Db 561 EEIEAEDDDSVVVTLVPKFGA--VKIGGIKIE 590

<!--EndFragment-->

<!--StartFragment-->RESULT 10

S33540

catechol oxidase (EC 1.10.3.1) B precursor [similarity] - tomato

C;Species: Lycopersicon esculentum (tomato)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-Oct-2004

C;Accession: S33540; S22966

R;Newman, S.M.; Eannetta, N.T.; Yu, H.; Prince, J.P.; de Vicente, C.; Tanksley, S.D.;

Plant Mol. Biol. 21, 1035-1051, 1993

A;Title: Organisation of the tomato polyphenol oxidase gene family.

A;Reference number: S33539; MUID:93257620; PMID:8098228

A;Accession: S33540

A;Molecule type: DNA

A;Residues: 1-596 <NEW>

A;Cross-references: UNIPROT:Q08304; UNIPARC:UPI00001320D7; EMBL:Z12834; NID:g1403351;

C;Superfamily: polyphenol oxidase, plant type

C;Keywords: oxidoreductase

F;199,208/Binding site: copper (His) #status predicted

F;329,333,371/Binding site: copper (His) #status predicted

Query Match 36.5%; Score 1184; DB 1; Length 596;
 Best Local Similarity 41.8%; Pred. No. 7.8e-83;
 Matches 272; Conservative 86; Mismatches 192; Indels 100; Gaps 24;

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Qy      1 MASLAL-SSLPTSTTTKKPLFSKTS SHVKP----FH-----REKVSCNAPADNNDKTVNN 50
      |||:  || |:|||| | |:  | ||  | ||||  | :||
Db      1 MASVVCNSSSSTTTTLKTPFTSLGSTPKPSQLFLHGKRNKTFKVSC-----KVINN 52

Qy      51 SDTPKLILPKTPLETQNVDRNLLGLGGLYGAANLTIP-SAFGIPIAAPDNISDCVAA 109
      :      || :||||:||||||| ||  || :|  || :|| : | |
Db      53 NGNQD-----ETNSVDRNVLLGLGGLYGVAN--AIPLAASATPIPSPD-LKTCGRA 101

Qy      110 TSNLRNSKDAIRGLACCPVLSTNKPMD----YVLPSPNVIRVRPAAQKATADYTAKYQQ 165
      |  |  :  :||| : ||  |  |  ||  :||  |  :|||
Db      102 TI----SDGPLVPYSCPPMPTN--FDTPYKFPSTKLRIPTAHAVDEEYIAKYNL 155

Qy      166 AIQAMKOLPED---HPHSWKQQGKIHCAYCNGGYNQEQSGYPNLQLQIHNSWLFFPFHRW 222
      || |:|| :  :| :||| ||||| |  :||:|||||||
Db      156 AISRMRDLDKTEPLNPLGFKQQANIHCAYCNGAYI-----IGGKELQVHNSWLFFPFHRW 210

Qy      223 YLYFYEKILGKLINDPTFALPYWNWDNPTGMVIPAMFEQNSKTNSLFDPLRDAKHLPPSI 282
      |||||:|||||:|||||||:| || :| ||::  :||:| | :  ::
Db      211 YLYFYERILGKLIDDPTFALPYWNWDHPKGMRLPPMFDREG--SSLYDERRNQQVRNGTV 268

Qy      283 FDVEYAGADTGATCIDQIAINLSSMYRQMVNTSTDTKRFFGGGEFVAGNDPLASEFNVAGT 342
      |:  |  | :  :: ||: |||||:  ||| :| ||:  ||
Db      269 LDLSFGDKVETTQLQLMSNNLTLMYRQMVNAPCPLLFFGAPYVLGNN-----VEAPGT 323

Qy      343 VEAGVHTAAHRWVG-----NSRMANSEDMGNFYSGYDPLFYVHHANVDRMWQIWKD 394
      :|  |  |||  |  ::  ||||| ||:|| || ||||| ||
Db      324 IETIPHIPVHIWAGTVRGSKFPNGDVSYGEDMGNFYSGLDPVFYCHHGNDVDRMWNEWKA 383

Qy      395 IDKKT HKDPTSGDWLNASYVFYDENENLVRVYNRDCVDINRMGYDYERSAIPWIRS RPTA 454
      |  |  :| :  |||: :  |||::| || |||:| :|||  ||  :|
Db      384 IGGK-RRDISEKDWLNSEFFFYDEHKNPYRVKVRDCLDTKKMGYDYAPMPTPWRNFKP-- 440

Qy      455 HAKGANVAAKSAGIVQKVE-----DIVFPL-KLNKIVKVLVKRPATNRTKEGKEKANE 506
      ||  |||  : ||| |::| :  : |||:|::| : |  |
Db      441 -----KSKASVGKVNTSTLPPANEVFLAKMDKTISFAINRPASSRTQQEKNEQEE 491

Qy      507 LLFVNGITFDAERFLKIDVFVNDVDDGIQTAAAD-SEFAGSFAQLPHNHGDKMFMRSGA- 564
      :|  |  | :|  :: |||:| ||:  |  :|||: ||| |  |:|

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Db 492 MLTFNNIRYDNRGYIRFDVFLN-VDNNVNaNELDKAEFAGSYTSLPHVH-----RAGEN 544

Qy 565 -----AFGITELLEDIEAEGDDSVVVTLVPRTGCDEVTIGEIKIQLV 606

||||||| | :|:: ||||: | : ::| ::|:|

Db 545 DHIKVNFLAITELLEDIGLEDEDTIAVTLVPKKGEGISIENVEIKLV 594

<!--EndFragment-->